

SEQUENCE LISTING

<110> Zhang, Lian Hui
Lin, Yi Han
Xu, Jin Liang

<120> Ralstonia AHL-Acylase Gene

<130> 2977-154

<140> 10/502351

<141> 2004-07-23

<150> PCT/SG02/000011

<151> 2002-01-23

<160> 7

<170> PatentIn version 3.3

<210> 1

<211> 3743

<212> DNA

<213> Ralstonia sp.

<220>

<221> misc_feature

<222> (16)..(16)

<223> n is a, c, g, or t

<400> 1

```
gtttgggaaa gtgggnagcg cgctgtgcag cgccccgccc ctacagccgcg cagctcggcg      60
cgcaccgaat gcgcgcgcgcg gtggggcgccc ggcggtgctggc cgggtgtggcg ccggatcagg      120
cgccggaagg cggacatgtc gtgataaccg cactgttcgg cgattgccgt caggctcagc      180
gtgctgactt ccagcaggtg gcaggcgcg cccacgcgca gccggtgcag caattgcagc      240
ggcgaggtgc ccagggtctt ggtgaaatgc cgcagcagcg tgcgctcgct ggtcgaggcg      300
gcggcgggcca gcttggccag gtcgaacggc tcgtgcaggt gctgctgcag gtagcgccgc      360
gcccgtagta ccacgttgtt gcggatggcg ggcttgctgc gcagccagat ggcggtggac      420
tcaccgcgcg acgggtggtc gagcacggcc tggccgaggg tgcgtgccag ccgggtgtcg      480
gccaggcggc cgaccaggcg ctgctgagc gccacgccgt gctccatcgc gcgcgccgtc      540
agcacgttgc cgctgctgac gatggcctgc tccgccacca ctttcagctg cgggtagttg      600
ccgtgcagcc agccggcgat cagccacgtc accgtcaagc gccggccggc gggcagcgcg      660
ccggccagca gcgccacgcc ggtgaaggac gaggccacca agcctgccgg cgtccaggta      720
```

gcgccggatg	gtggcgcggt	cccactccag	cagggccagg	cgctgctcca	gcgtgctgat	780
gtggtcgaaa	tgcaggggcg	ggacgaccag	cgctcgccc	agcgcggcgt	cgcccgccgg	840
cagcggctgg	cagcggcagg	ccagggctct	ggcggcggcc	tgccagcggg	ccgggtcgcg	900
cgcgaccagc	cgccacccga	acaccgggct	ggcggcatcg	gcacgcttgc	cggcatgcat	960
ggaggcgagc	gcattggcca	cgccgagggg	gtcggcgacg	gtcgccagcg	tggagaggcc	1020
ggcgctcgga	aaggtcagca	ggtcgatgtc	ggcatccgca	aagtataggg	gaggcgggcg	1080
gaggcctcct	gcgtggcggg	attgacccca	actctggcgg	gaatacctct	ttcctccggg	1140
cgggccccag	tcgacgatac	ggcgggtggct	gcgcctgcgc	gccgccgcaa	gactagagcg	1200
acacaagaca	agaccgacaa	caggagacaa	cgcatgatgc	agggatctgc	gctgcgcggc	1260
acgctcgcca	tggccgcgct	cgcggcgctg	gccggctgcg	ccagttccac	cgatggccgc	1320
tgggggtcgc	tcagcgacac	cggcctgtcc	gccgagatcc	gccgcaccgg	cttcggcatt	1380
ccgcacatcc	gcgccaacga	ctacgccagc	ctcggctatg	gcattggccta	tgctacgcg	1440
caggacaacc	tgtgcctgct	ggccgaccag	gtggtcaccg	tcaacggcga	gcgctcgaag	1500
accttcgggc	ccgagggcac	cgtgacggtc	tcgttcaagc	cgatcccca	cctgcagtcg	1560
gacgccttct	tcaagggcat	cttcgacgag	gacggcctgc	gcgccggtta	tgcgagatg	1620
tcgcccagag	cgcgcgagct	gctgcgcggc	tacatcgccg	gcttcaaccg	ctatctcaag	1680
gacacgccgc	ccgccaactt	cccggccgcc	tgccgcaatg	ccgcctgggt	gcgtccgctc	1740
acgctgggcg	acatgatgcg	catgggcgaa	gagaaggcga	tccaggccag	cgccggcgcc	1800
atgctggcgg	gcattcgctc	cgcgagccg	ccgggccgca	cgccggtggc	cgagcgcgag	1860
attccgccgc	aggccgtcga	caccgtggcg	ctggaccgcg	aactgcagct	gcgcgacatg	1920
ccgatcggct	ccaacggctg	ggccttcggc	gctgacgcca	ccgcccaaccg	gcgcggcggtg	1980
ctgctcggca	atccgcactt	cccgtggacg	accaccaacc	gcttctacca	ggtccacctg	2040
acggtgcccc	gcaagctcga	cgtgatgggc	gcctcgatcg	cggccttccc	ggtggtgagc	2100
atcggcttca	acaaggacgt	ggcgtggacg	cacaccgtct	ccaccggccg	ccgcttcacc	2160
ttgttcgaac	tgaagctggc	cgaaggcgac	ccgaccacct	acctggtcga	cggcacgccg	2220
cacaagatga	ccaccgcac	ggtcgccttc	gacgtcaagc	tgccggacgg	ccgcctcgag	2280
cgccgcacgc	acaccttcta	cgacaccatc	tacggcccgg	tgctgtcgat	gccgagcggc	2340

ggcatgccgt ggaccacgca gaaggcctac gccctgcgcg acgccaaccg caacaacacg	2400
cgctcgggtcg acagctggct gcatatcggg caggccccgg acgtggccgg catccgccag	2460
gccatcggca acctgggcat tccctgggtc aacaccatcg ccaccgaccg caacggccgc	2520
gcgctgttcg ccgacgtgtc gaccacgccg gacgtgccgg ccgcggagct ccagcgctgt	2580
gccccgtcgc cgctggccgg caaactcttc aaggacgcgg gcctggtgct gctcgacggc	2640
tcgcgcggca cctgcaactg gcaggtcgat ccggcttcgc cggtaccggg gctggtggcg	2700
cccgcgcgca tgccggtgct cgagcgcgac gactacgtcg ccaacagcaa tgacagctcc	2760
tggtgacca accccgcgca aaagctgacc ggcttctcgc cggtgatggg ctcggtcgac	2820
gtaccgcagc ggctgcgcac gcgcacggc ctgatcgaga tcggccgccc cctggccggc	2880
accgacggac tgcccggcaa ccgcacgat ctgccgaacc tgcaggcgat gatcttcagc	2940
aatgccaacc tggcgggaca actggtgctg ggcgacctgc tcgcggcatg caaggccacg	3000
ccggccccgg atgccgacgt gcgcgacggc tgcgccgcc tcggccagtg gaaccgcacc	3060
agcaacgccg acgcccgcgc cgcgcacctg ttccgcgagt tctggatgcg cgccaaggac	3120
atcgcgcagg tgcacgccgt cgagttcgac ccggccgacc cggtcacac gccgcgcggc	3180
ctgcgcacga acgacgcgac ggtacgcacg gcggtgttca aggcgctgaa ggaagccgtg	3240
ggcgcggtgc gcaaggcggg cttcgcgctg gatgcgccgc tgggcacggg acaggccgcg	3300
cacgcaccgg acggctccat cgccctgcac ggccggcgagg aatacgaagg cgtgctcaac	3360
aagctgcaaa ccctgccgat cgggccgaag gggctgccgg tgtatttcgg caccagctac	3420
atccagaccg tgaccttcga cgaccagggc ccggtcgccg acgccatcct cacctacggc	3480
gaatcgaccg accacgcctc gccgcacgcg ttcgaccaga tgcgtgcgta ctcgggcaag	3540
cactggaacc ggctgccgtt ctccgaagcg gccatcgccg ccgatccggc gctgaagggtg	3600
atgcggttgt cgcagtgagg gctgccggtg cctggaaaaa cgccccgctt gtgcggggcg	3660
tttttttgcc agtgtgaatg gctcaatcgt gttggaaacc gcatccggac atgactgtat	3720
tgtgactctg cctgtgtccg tgt	3743

<210> 2
 <211> 794
 <212> PRT
 <213> *Ralstonia* sp.

<400> 2

Met Met Gln Gly Phe Ala Leu Arg Gly Thr Leu Ala Met Ala Ala Leu
 1 5 10 15

Ala Ala Leu Ala Gly Cys Ala Ser Ser Thr Asp Gly Arg Trp Gly Ser
 20 25 30

Leu Ser Asp Thr Gly Leu Ser Ala Glu Ile Arg Arg Thr Gly Phe Gly
 35 40 45

Ile Pro His Ile Arg Ala Asn Asp Tyr Ala Ser Leu Gly Tyr Gly Met
 50 55 60

Ala Tyr Ala Tyr Ala Gln Asp Asn Leu Cys Leu Leu Ala Asp Gln Val
 65 70 75 80

Val Thr Val Asn Gly Glu Arg Ser Lys Thr Phe Gly Pro Glu Gly Thr
 85 90 95

Val Thr Val Ser Phe Lys Pro Ile Pro Asn Leu Gln Ser Asp Ala Phe
 100 105 110

Phe Lys Gly Ile Phe Asp Glu Asp Gly Leu Arg Ala Gly Tyr Ala Gln
 115 120 125

Met Ser Pro Glu Ala Arg Glu Leu Leu Arg Gly Tyr Ile Ala Gly Phe
 130 135 140

Asn Arg Tyr Leu Lys Asp Thr Pro Pro Ala Asn Phe Pro Ala Ala Cys
 145 150 155 160

Arg Asn Ala Ala Trp Val Arg Pro Leu Thr Leu Gly Asp Met Met Arg
 165 170 175

Met Gly Glu Glu Lys Ala Ile Gln Ala Ser Ala Gly Ala Met Leu Ala
 180 185 190

Gly Ile Val Ala Ala Gln Pro Pro Gly Arg Thr Pro Val Ala Glu Arg
 195 200 205

Glu Ile Pro Pro Gln Ala Val Asp Thr Val Ala Leu Asp Arg Glu Leu
 210 215 220

Gln Leu Arg Asp Met Pro Ile Gly Ser Asn Gly Trp Ala Phe Gly Ala
 225 230 235 240

Asp Ala Thr Ala Asn Arg Arg Gly Val Leu Leu Gly Asn Pro His Phe
 245 250 255

Pro Trp Thr Thr Thr Asn Arg Phe Tyr Gln Val His Leu Thr Val Pro
 260 265 270

Gly Lys Leu Asp Val Met Gly Ala Ser Ile Ala Ala Phe Pro Val Val
 275 280 285

Ser Ile Gly Phe Asn Lys Asp Val Ala Trp Thr His Thr Val Ser Thr
 290 295 300

Gly Arg Arg Phe Thr Leu Phe Glu Leu Lys Leu Ala Glu Gly Asp Pro
 305 310 315 320

Thr Thr Tyr Leu Val Asp Gly Thr Pro His Lys Met Thr Thr Arg Thr
 325 330 335

Val Ala Phe Asp Val Lys Leu Pro Asp Gly Arg Leu Glu Arg Arg Thr
 340 345 350

His Thr Phe Tyr Asp Thr Ile Tyr Gly Pro Val Leu Ser Met Pro Ser
 355 360 365

Gly Gly Met Pro Trp Thr Thr Gln Lys Ala Tyr Ala Leu Arg Asp Ala
 370 375 380

Asn Arg Asn Asn Thr Arg Ser Val Asp Ser Trp Leu His Ile Gly Gln
 385 390 395 400

Ala Arg Asp Val Ala Gly Ile Arg Gln Ala Ile Gly Asn Leu Gly Ile
 405 410 415

Pro Trp Val Asn Thr Ile Ala Thr Asp Arg Asn Gly Arg Ala Leu Phe
 420 425 430

Ala Asp Val Ser Thr Thr Pro Asp Val Pro Ala Ala Glu Leu Gln Arg
 435 440 445

Cys Ala Pro Ser Pro Leu Ala Gly Lys Leu Phe Lys Asp Ala Gly Leu
 450 455 460

Val Leu Leu Asp Gly Ser Arg Gly Thr Cys Asn Trp Gln Val Asp Pro
 465 470 475 480

Ala Ser Pro Val Pro Gly Leu Val Ala Pro Ala Arg Met Pro Val Leu
 485 490 495

Glu Arg Asp Asp Tyr Val Ala Asn Ser Asn Asp Ser Ser Trp Leu Thr
 500 505 510

Asn Pro Ala Gln Lys Leu Thr Gly Phe Ser Pro Val Met Gly Ser Val
 515 520 525

Asp Val Pro Gln Arg Leu Arg Thr Arg Ile Gly Leu Ile Glu Ile Gly
 530 535 540

Arg Arg Leu Ala Gly Thr Asp Gly Leu Pro Gly Asn Arg Ile Asp Leu
 545 550 555 560

Pro Asn Leu Gln Ala Met Ile Phe Ser Asn Ala Asn Leu Ala Gly Gln
 565 570 575

Leu Val Leu Gly Asp Leu Leu Ala Ala Cys Lys Ala Thr Pro Ala Pro
 580 585 590

Asp Ala Asp Val Arg Asp Gly Cys Ala Ala Leu Gly Gln Trp Asn Arg
 595 600 605

Thr Ser Asn Ala Asp Ala Arg Ala Ala His Leu Phe Arg Glu Phe Trp
 610 615 620

Met Arg Ala Lys Asp Ile Ala Gln Val His Ala Val Glu Phe Asp Pro
 625 630 635 640

Ala Asp Pro Val His Thr Pro Arg Gly Leu Arg Met Asn Asp Ala Thr
 645 650 655

Val Arg Thr Ala Val Phe Lys Ala Leu Lys Glu Ala Val Gly Ala Val
 660 665 670

Arg Lys Ala Gly Phe Ala Leu Asp Ala Pro Leu Gly Thr Val Gln Ala
675 680 685

Ala His Ala Pro Asp Gly Ser Ile Ala Leu His Gly Gly Glu Glu Tyr
690 695 700

Glu Gly Val Leu Asn Lys Leu Gln Thr Leu Pro Ile Gly Pro Lys Gly
705 710 715 720

Leu Pro Val Tyr Phe Gly Thr Ser Tyr Ile Gln Thr Val Thr Phe Asp
725 730 735

Asp Gln Gly Pro Val Ala Asp Ala Ile Leu Thr Tyr Gly Glu Ser Thr
740 745 750

Asp His Ala Ser Pro His Ala Phe Asp Gln Met Arg Ala Tyr Ser Gly
755 760 765

Lys His Trp Asn Arg Leu Pro Phe Ser Glu Ala Ala Ile Ala Ala Asp
770 775 780

Pro Ala Leu Lys Val Met Arg Leu Ser Gln
785 790

<210> 3
<211> 785
<212> PRT
<213> Deinococcus radiodurans

<400> 3

Met Ser Arg Ser Pro Phe Ser Ser Val Ser Leu Pro Ala Arg Leu Leu
1 5 10 15

Leu Gly Ser Leu Leu Leu Gly Pro Leu Met Leu Gly Gly Ala Ala Ser
20 25 30

Ala Gln Thr Tyr Gln Val Gln Ile Gln Arg Thr Ala His Gly Ile Pro
35 40 45

His Ile Gln Ala Ser Asp Leu Gly Gly Ile Gly Tyr Gly Val Gly Tyr
50 55 60

Ser Tyr Ala Gln Asp Asn Leu Cys Leu Leu Ala Asp Gln Val Met Thr
65 70 75 80

Val Arg Gly Glu Arg Ser Lys Phe Leu Gly Ala Glu Gly Lys Thr Val
85 90 95

Val Gly Phe Gln Pro Val Asn Asn Leu Asp Ser Asp Val Phe Phe Lys
100 105 110

Thr Val Ile Glu Pro Gly Arg Leu Gln Ala Gly Tyr Arg Asp Gln Pro
115 120 125

Gln Ile Leu Ala Leu Met Arg Gly Tyr Val Ala Gly Val Asn Arg Tyr
130 135 140

Leu Arg Asp Thr Pro Pro Glu Gln Trp Pro Ser Ala Cys Arg Asn Ala
145 150 155 160

Asp Trp Val Arg Pro Leu Thr Glu Leu Asp Val Met Arg Leu Gly Glu
165 170 175

Glu Lys Ala Ile Gln Ala Ser Ala Gly Ala Met Val Ser Ala Ile Thr
180 185 190

Ser Ala Arg Pro Pro Gln Ala Gly Ala Ser Thr Ala Ala Pro Arg Pro
195 200 205

Asp Leu Ala Ala Phe Asn Arg Gln Tyr Arg Phe Asn Asp Leu Pro Ile
210 215 220

Gly Ser Asn Gly Trp Ala Phe Gly Ser Glu Ala Thr Thr Asn Gly Arg
225 230 235 240

Gly Leu Leu Leu Gly Asn Pro His Phe Pro Trp Glu Thr Ser Asn Arg
245 250 255

Phe Tyr Gln Leu His Leu Thr Leu Pro Gly Gln Phe Asp Val Met Gly
260 265 270

Ala Ser Leu Gly Gly Met Pro Val Val Asn Ile Gly Phe Asn Gln Asp
275 280 285

Val Ala Trp Thr His Thr Val Ser Thr Asp Lys Arg Phe Thr Leu Ala
 290 295 300

Ala Leu Thr Leu Val Pro Gly Asp Pro Leu Ser Tyr Val Lys Asp Gly
 305 310 315 320

Gln Gln Arg Arg Leu Gln Arg Arg Thr Ala Val Ile Glu Val Lys Thr
 325 330 335

Ala Asn Gly Pro Arg Leu His Thr Arg Thr Val Tyr Phe Thr Pro Glu
 340 345 350

Gly Pro Leu Val Asn Leu Pro Ala Ala Gly Leu Thr Trp Thr Pro Gln
 355 360 365

Tyr Ala Phe Ala Leu Arg Asp Ala Asn Arg Asn Asn Thr Arg Met Leu
 370 375 380

Ala Thr Trp Leu Gly Phe Ala Gly Ala Lys Ser Val Arg Asp Ile Arg
 385 390 395 400

Ala Ser Leu Asn Val Gln Gly Ile Pro Trp Val Asn Thr Ile Ala Ala
 405 410 415

Asp Arg Ala Gly Ser Ala Leu Tyr Ala Asp Ile Ser Ser Ser Pro Asn
 420 425 430

Val Ser Ala Ala Gln Gln Gln Ala Cys Thr Pro Pro Pro Leu Ala Pro
 435 440 445

Leu Phe Pro Ala Ala Gly Leu Ala Val Leu Asp Gly Ser His Ser Ala
 450 455 460

Cys Asp Trp Lys Thr Asp Pro Ala Ser Arg Val Pro Gly Leu Arg Ala
 465 470 475 480

Pro Asp Lys Met Pro Val Leu Ile Arg Gln Asp Phe Val Ala Asn Ser
 485 490 495

Asn Asn Ser Ala Trp Leu Ala Asn Pro Ala Ala Pro Gln Thr Gly Leu
 500 505 510

Asp Pro Leu Val Gly Glu Val Asn Ala Pro Gln Ser Pro Arg Thr Arg
515 520 525

Met Gly Leu Leu Glu Ile Gly Arg Arg Leu Ser Gly Thr Asp Gly Leu
530 535 540

Pro Gly Arg Thr Phe Asp Ile Pro Thr Leu Gln Ala Thr Leu Leu Arg
545 550 555 560

Glu Ser Asn Leu Thr Gly Glu Met Tyr Ala Ala Asp Ala Ala Lys Leu
565 570 575

Cys Gln Ser Ala Gly Gly Ala Glu Leu Gln Pro Ala Cys Asn Ala Leu
580 585 590

Ala Ala Trp Asp Arg Arg Ser Ser Gln Glu Ser Arg Gly Ala Ala Leu
595 600 605

Trp Arg Glu Phe Trp Arg Arg Ala Arg Ala Ile Pro Asn Val Tyr Ala
610 615 620

Val Pro Phe Asp Pro Ala Asp Pro Val Asn Thr Pro Arg Gly Leu Asn
625 630 635 640

Thr Ala Asp Pro Ala Ala Gln Thr Ala Leu Leu Gly Ala Leu Arg Glu
645 650 655

Ala Ala Ala Ala Leu Thr Ala Ala Gly Ile Pro Phe Asp Ala Pro Leu
660 665 670

Gly Glu Val Gln Gly Val Val Arg Gly Gly Asp Phe Ile Ser Leu Pro
675 680 685

Gly Gly Ala Glu Phe Glu Gly Val Leu Asp Lys Ile Asp Phe Asn Pro
690 695 700

Leu Ala Pro Gly Gly Tyr Arg Gly Val Val Gly Asn Ala Ser Ser Tyr
705 710 715 720

Ile Gln Thr Val Gly Phe Thr Asp Ser Gly Val Gln Ala Glu Ala Val
725 730 735

Leu Thr Tyr Ser Gln Ser Ser Asn Pro Glu Ser Pro Tyr Phe Ser Asp
740 745 750

Gln Thr Arg Leu Phe Ser Arg Ser Glu Trp Val Lys Leu Pro Phe Thr
755 760 765

Gln Pro Glu Ile Glu Ala Asp Pro Thr Arg Thr Val Val Gln Leu Ser
770 775 780

Glu
785

<210> 4
<211> 786
<212> PRT
<213> Actinoplanes utahensis

<400> 4

Met Thr Ser Ser Tyr Met Arg Leu Lys Ala Ala Ala Ile Ala Phe Gly
1 5 10 15

Val Ile Val Ala Thr Ala Ala Val Pro Ser Pro Ala Ser Gly Arg Glu
20 25 30

His Asp Gly Gly Tyr Ala Ala Leu Ile Arg Arg Ala Ser Tyr Gly Val
35 40 45

Pro His Ile Thr Ala Asp Asp Phe Gly Ser Leu Gly Phe Gly Val Gly
50 55 60

Tyr Val Gln Ala Glu Asp Asn Ile Cys Val Ile Ala Glu Ser Val Val
65 70 75 80

Thr Ala Asn Gly Glu Arg Ser Arg Trp Phe Gly Ala Thr Gly Pro Asp
85 90 95

Asp Ala Asp Val Arg Thr Thr Ser Ser Thr Gln Ala Ile Asp Asp Arg
100 105 110

Val Ala Glu Arg Leu Leu Glu Gly Pro Arg Asp Gly Val Arg Ala Pro
115 120 125

Cys Asp Asp Val Arg Asp Gln Met Arg Gly Phe Val Ala Gly Tyr Asn
 130 135 140

His Phe Leu Arg Arg Thr Gly Val His Arg Leu Thr Asp Pro Ala Cys
 145 150 155 160

Arg Gly Lys Ala Trp Val Arg Pro Leu Ser Glu Ile Asp Leu Trp Arg
 165 170 175

Thr Ser Trp Asp Ser Met Val Arg Ala Gly Ser Gly Ala Leu Leu Asp
 180 185 190

Gly Ile Val Ala Ala Thr Pro Pro Thr Ala Ala Gly Pro Ala Ser Ala
 195 200 205

Pro Glu Ala Pro Asp Ala Ala Ala Ile Ala Ala Ala Leu Asp Gly Thr
 210 215 220

Ser Ala Gly Ile Gly Ser Asn Ala Tyr Gly Leu Gly Ala Gln Ala Thr
 225 230 235 240

Val Asn Gly Ser Gly Met Val Leu Ala Asn Pro His Phe Pro Trp Gln
 245 250 255

Gly Ala Glu Arg Phe Tyr Arg Met His Leu Lys Val Pro Gly Arg Tyr
 260 265 270

Asp Val Glu Gly Ala Ala Leu Ile Gly Asp Pro Ile Ile Glu Ile Gly
 275 280 285

His Asn Arg Thr Val Ala Trp Ser His Thr Val Ser Thr Ala Arg Arg
 290 295 300

Phe Val Trp His Arg Leu Ser Leu Val Pro Gly Asp Pro Thr Ser Tyr
 305 310 315 320

Tyr Val Asp Gly Arg Pro Glu Arg Met Arg Ala Arg Thr Val Thr Val
 325 330 335

Gln Thr Gly Ser Gly Pro Val Ser Arg Thr Phe His Asp Thr Arg Tyr
 340 345 350

Gly Pro Val Ala Val Val Pro Gly Thr Phe Asp Trp Thr Pro Ala Thr
 355 360 365

Ala Tyr Ala Ile Thr Asp Val Asn Ala Gly Asn Asn Arg Ala Phe Asp
 370 375 380

Gly Trp Leu Arg Met Gly Gln Ala Lys Asp Val Arg Ala Leu Lys Ala
 385 390 395 400

Val Leu Asp Arg His Gln Phe Leu Pro Trp Val Asn Val Ile Ala Ala
 405 410 415

Asp Ala Arg Gly Glu Ala Leu Tyr Gly Asp His Ser Val Val Pro Arg
 420 425 430

Val Thr Gly Ala Leu Ala Ala Ala Cys Ile Pro Ala Pro Phe Gln Pro
 435 440 445

Leu Tyr Ala Ser Ser Gly Gln Ala Val Leu Asp Gly Ser Arg Ser Asp
 450 455 460

Cys Ala Leu Gly Ala Asp Pro Asp Ala Ala Val Pro Gly Ile Leu Gly
 465 470 475 480

Pro Ala Ser Leu Pro Val Arg Phe Arg Asp Asp Tyr Val Thr Asn Ser
 485 490 495

Asn Asp Ser His Trp Leu Ala Ser Pro Ala Ala Pro Leu Glu Gly Phe
 500 505 510

Pro Arg Ile Leu Gly Asn Glu Arg Thr Pro Arg Ser Leu Arg Thr Arg
 515 520 525

Leu Gly Leu Asp Gln Ile Gln Gln Arg Leu Ala Gly Thr Asp Gly Leu
 530 535 540

Pro Gly Lys Gly Phe Thr Thr Ala Arg Leu Trp Gln Val Met Phe Gly
 545 550 555 560

Asn Arg Met His Gly Ala Glu Leu Val Arg Asp Asp Leu Val Ala Leu
 565 570 575

Cys Arg Arg Gln Pro Thr Ala Thr Ala Ser Asn Gly Ala Ile Val Asp
580 585 590

Leu Thr Ala Ala Cys Thr Ala Leu Ser Arg Phe Asp Glu Arg Ala Asp
595 600 605

Leu Asp Ser Arg Gly Ala His Leu Phe Thr Glu Phe Leu Ala Gly Gly
610 615 620

Ile Arg Phe Ala Asp Thr Phe Glu Val Thr Asp Pro Val Arg Thr Pro
625 630 635 640

Ala Pro Phe Trp Asn Thr Thr Asp Pro Arg Val Arg Thr Ala Leu Ala
645 650 655

Asp Ala Cys Asn Gly Ser Pro Ala Ser Pro Ser Thr Arg Ser Val Gly
660 665 670

Asp Ile His Thr Asp Ser Arg Gly Glu Arg Arg Ile Pro Ile His Gly
675 680 685

Gly Arg Gly Glu Ala Gly Thr Phe Asn Val Ile Thr Asn Pro Leu Val
690 695 700

Pro Gly Val Gly Tyr Pro Gln Val Val His Gly Thr Ser Phe Val Met
705 710 715 720

Ala Val Glu Leu Gly Pro His Gly Pro Ser Gly Arg Gln Ile Leu Thr
725 730 735

Tyr Ala Gln Ser Thr Asn Pro Asn Ser Pro Trp Tyr Ala Asp Gln Thr
740 745 750

Val Leu Tyr Ser Arg Lys Gly Trp Asp Thr Ile Lys Tyr Thr Glu Ala
755 760 765

Gln Ile Ala Ala Asp Pro Asn Leu Arg Val Tyr Arg Val Ala Gln Arg
770 775 780

Gly Arg
785

<210> 5
 <211> 777
 <212> PRT
 <213> *Pseudomonas aeruginosa*

<400> 5

Met Ser Arg Pro Phe Arg Pro Pro Leu Cys Arg Glu Thr Thr Ser Met
 1 5 10 15

Gly Met Arg Thr Val Leu Thr Gly Leu Ala Gly Met Leu Leu Gly Ser
 20 25 30

Met Met Pro Val Gln Ala Asp Met Pro Arg Pro Thr Gly Leu Ala Ala
 35 40 45

Asp Ile Arg Trp Thr Ala Tyr Gly Val Pro His Ile Arg Ala Lys Asp
 50 55 60

Glu Arg Gly Leu Gly Tyr Gly Ile Gly Tyr Ala Tyr Ala Arg Asp Asn
 65 70 75 80

Ala Cys Leu Leu Ala Glu Glu Ile Val Thr Ala Arg Gly Glu Arg Ala
 85 90 95

Arg Tyr Phe Gly Ser Glu Gly Lys Ser Ser Ala Glu Leu Asp Asn Leu
 100 105 110

Pro Ser Asp Ile Phe Tyr Ala Trp Leu Asn Gln Pro Glu Ala Leu Gln
 115 120 125

Ala Phe Trp Gln Ala Gln Thr Pro Ala Val Arg Gln Leu Leu Glu Gly
 130 135 140

Tyr Ala Ala Gly Phe Asn Arg Phe Leu Arg Glu Ala Asp Gly Lys Thr
 145 150 155 160

Thr Ser Cys Leu Gly Gln Pro Trp Leu Arg Ala Ile Ala Thr Asp Asp
 165 170 175

Leu Leu Arg Leu Thr Arg Arg Leu Leu Val Glu Gly Gly Val Gly Gln
 180 185 190

Phe Ala Asp Ala Leu Val Ala Ala Ala Pro Pro Gly Ala Glu Lys Val
195 200 205

Ala Leu Ser Gly Glu Gln Ala Phe Gln Val Ala Glu Gln Arg Arg Gln
210 215 220

Arg Phe Arg Leu Glu Arg Gly Ser Asn Ala Ile Ala Val Gly Ser Glu
225 230 235 240

Arg Ser Ala Asp Gly Lys Gly Met Leu Leu Ala Asn Pro His Phe Pro
245 250 255

Trp Asn Gly Ala Met Arg Phe Tyr Gln Met His Leu Thr Ile Pro Gly
260 265 270

Arg Leu Asp Val Met Gly Ala Ser Leu Pro Gly Leu Pro Val Val Asn
275 280 285

Ile Gly Phe Ser Arg His Leu Ala Trp Thr His Thr Val Asp Thr Ser
290 295 300

Ser His Phe Thr Leu Tyr Arg Leu Ala Leu Asp Pro Lys Asp Pro Arg
305 310 315 320

Arg Tyr Leu Val Asp Gly Arg Ser Leu Pro Leu Glu Glu Lys Ser Val
325 330 335

Ala Ile Glu Val Arg Gly Ala Asp Gly Lys Leu Ser Arg Val Glu His
340 345 350

Lys Val Tyr Gln Ser Ile Tyr Gly Pro Leu Val Val Trp Pro Gly Lys
355 360 365

Leu Asp Trp Asn Arg Ser Glu Ala Tyr Ala Leu Arg Asp Ala Asn Leu
370 375 380

Glu Asn Thr Arg Val Leu Gln Gln Trp Tyr Ser Ile Asn Gln Ala Ser
385 390 395 400

Asp Val Ala Asp Leu Arg Arg Arg Val Glu Ala Leu Gln Gly Ile Pro
405 410 415

Trp Val Asn Thr Leu Ala Ala Asp Glu Gln Gly Asn Ala Leu Tyr Met
420 425 430

Asn Gln Ser Val Val Pro Tyr Leu Lys Pro Glu Leu Ile Pro Ala Cys
435 440 445

Ala Ile Pro Gln Leu Val Ala Glu Gly Leu Pro Ala Leu Gln Gly Gln
450 455 460

Asp Ser Arg Cys Ala Trp Ser Arg Asp Pro Ala Ala Ala Gln Ala Gly
465 470 475 480

Ile Thr Pro Ala Ala Gln Leu Pro Val Leu Leu Arg Arg Asp Phe Val
485 490 495

Gln Asn Ser Asn Asp Ser Ala Trp Leu Thr Asn Pro Ala Ser Pro Leu
500 505 510

Gln Gly Phe Ser Pro Leu Val Ser Gln Glu Lys Pro Ile Gly Pro Arg
515 520 525

Ala Arg Tyr Ala Leu Ser Arg Leu Gln Gly Lys Gln Pro Leu Glu Ala
530 535 540

Lys Thr Leu Glu Glu Met Val Thr Ala Asn His Val Phe Ser Ala Asp
545 550 555 560

Gln Val Leu Pro Asp Leu Leu Arg Leu Cys Arg Asp Asn Gln Gly Glu
565 570 575

Lys Ser Leu Ala Arg Ala Cys Ala Ala Leu Ala Gln Trp Asp Arg Gly
580 585 590

Ala Asn Leu Asp Ser Gly Ser Gly Phe Val Tyr Phe Gln Arg Phe Met
595 600 605

Gln Arg Phe Ala Glu Leu Asp Gly Ala Trp Lys Glu Pro Phe Asp Ala
610 615 620

Gln Arg Pro Leu Asp Thr Pro Gln Gly Ile Ala Leu Asp Arg Pro Gln
625 630 635 640

Val Ala Thr Gln Val Arg Gln Ala Leu Ala Asp Ala Ala Ala Glu Val
645 650 655

Glu Lys Ser Gly Ile Pro Asp Gly Ala Arg Trp Gly Asp Leu Gln Val
660 665 670

Ser Thr Arg Gly Gln Glu Arg Ile Ala Ile Pro Gly Gly Asp Gly His
675 680 685

Phe Gly Val Tyr Asn Ala Ile Gln Ser Val Arg Lys Gly Asp His Leu
690 695 700

Glu Val Val Gly Gly Thr Ser Tyr Ile Gln Leu Val Thr Phe Pro Glu
705 710 715 720

Glu Gly Pro Lys Ala Arg Gly Leu Leu Ala Phe Ser Gln Ser Ser Asp
725 730 735

Pro Arg Ser Pro His Tyr Arg Asp Gln Thr Glu Leu Phe Ser Arg Gln
740 745 750

Gln Trp Gln Thr Leu Pro Phe Ser Asp Arg Gln Ile Asp Ala Asp Pro
755 760 765

Gln Leu Gln Arg Leu Ser Ile Arg Glu
770 775

<210> 6
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer for the QsbA gene

<400> 6
cgtggatcca tgatgcagga ttcgccgctg cgc

33

<210> 7
<211> 32
<212> DNA
<213> Artificial Sequence

<220>

<223> Reverse Primer for the QsbA gene

<400> 7

cgcgattca ccggcagccc tcatgcgaca ac

32